

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Jens Koßmann
- (B) STREET ADDRESS: Golmer Fichten 9
- (C) CITY: Golm
- (E) COUNTRY: DE
- (F) POSTAL CODE: 14476

(ii) TITLE OF INVENTION: Plants synthesizing a modified starch, methods for their production as well as modified starch

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER-READABLE VERSION:

- (A) DATA CARRIER: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4856 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Solanum tuberosum
- (B) STRAIN: C.V. Berolina

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 105..4497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CATCTTCATC GAATTTCTCG AAGCTTCTTC GCTAATTTC	60
TGGTTTCTTC ACTCAAATC	
GACGTTTCTA GCTGAACTTG AGTGAATTAA GCCAGTGGGA GGAT ATG AGT AAT TCC	116
Met Ser Asn Ser	
1	
TTA GGG AAT AAC TTG CTG TAC CAG GGA TTC CTA ACC TCA ACA GTG TTG	164
Leu Gly Asn Asn Leu Leu Tyr Gln Gly Phe Leu Thr Ser Thr Val Leu	
5 10 15 20	
GAA CAT AAA AGT AGA ATC AGT CCT CCT TGT GTT GGA GGC AAT TCT TTG	212
Glu His Lys Ser Arg Ile Ser Pro Pro Cys Val Gly Gly Asn Ser Leu	
25 30 35	

TTT	CAA	CAA	CAA	GTG	ATC	TCG	AAA	TCA	CCT	TTA	TCA	ACT	GAG	TTT	CGA	260
Phe	Gln	Gln	Gln	Val	Ile	Ser	Lys	Ser	Pro	Leu	Ser	Thr	Glu	Phe	Arg	
40								45				50				
GGT	AAC	AGG	TTA	AAG	GTG	CAG	AAA	AAG	AAA	ATA	CCT	ATG	GAA	AAG	AAG	308
Gly	Asn	Arg	Leu	Lys	Val	Gln	Lys	Lys	Lys	Ile	Pro	Met	Glu	Lys	Lys	
55								60				65				
CGT	GCT	TTT	TCT	AGT	TCT	CCT	CAT	GCT	GTA	CTT	ACC	ACT	GAT	ACC	TCT	356
Arg	Ala	Phe	Ser	Ser	Ser	Pro	His	Ala	Val	Leu	Thr	Thr	Asp	Thr	Ser	
70								75				80				
TCT	GAG	CTA	GCA	GAA	AAG	TTC	AGT	CTA	GGG	GGG	AAT	ATT	GAG	CTA	CAG	404
Ser	Glu	Leu	Ala	Glu	Lys	Phe	Ser	Leu	Gly	Gly	Asn	Ile	Glu	Leu	Gln	
85								90				95				
GTT	GAT	GTT	AGG	CCT	CCC	ACT	TCA	GGT	GAT	GTG	TCC	TTT	GTG	GAT	TTT	452
Val	Asp	Val	Arg	Pro	Pro	Thr	Ser	Gly	Asp	Val	Ser	Phe	Val	Asp	Phe	
105								110				115				
CAA	GTA	ACA	AAT	GGT	AGT	GAT	AAA	CTG	TTT	TTG	CAC	TGG	GGG	GCA	GTA	500
Gln	Val	Thr	Asn	Gly	Ser	Asp	Lys	Leu	Phe	Leu	His	Trp	Gly	Ala	Val	
120								125				130				
AAA	TTC	GGG	AAA	GAA	ACA	TGG	TCT	CTT	CCG	AAT	GAT	CGT	CCA	GAT	GGG	548
Lys	Phe	Gly	Lys	Glu	Thr	Trp	Ser	Leu	Pro	Asn	Asp	Arg	Pro	Asp	Gly	
135								140				145				
ACC	AAA	GTG	TAC	AAG	AAC	AAA	GCA	CTT	AGA	ACT	CCA	TTT	GTT	AAA	TCT	596
Thr	Lys	Val	Tyr	Lys	Asn	Lys	Ala	Leu	Arg	Thr	Pro	Phe	Val	Lys	Ser	
150								155				160				
GGC	TCT	AAC	TCC	ATC	CTG	AGA	CTG	GAG	ATA	CGA	GAC	ACT	GCT	ATC	GAA	644
Gly	Ser	Asn	Ser	Ile	Leu	Arg	Leu	Glu	Ile	Arg	Asp	Thr	Ala	Ile	Glu	
165								170				175				
GCT	ATT	GAG	TTT	CTC	ATA	TAC	GAT	GAA	GCC	CAC	GAT	AAA	TGG	ATA	AAG	692
Ala	Ile	Glu	Phe	Leu	Ile	Tyr	Asp	Glu	Ala	His	Asp	Lys	Trp	Ile	Lys	
185								190				195				
AAT	AAT	GGT	GGT	AAT	TTT	CGT	GTC	AAA	TTG	TCA	AGA	AAA	GAG	ATA	CGA	740
Asn	Asn	Gly	Gly	Asn	Phe	Arg	Val	Lys	Leu	Ser	Arg	Lys	Glu	Ile	Arg	
200								205				210				
GGC	CCA	GAT	GTT	TCT	GTT	CCT	GAG	GAG	CTT	GTA	CAG	ATC	CAA	TCA	TAT	788
Gly	Pro	Asp	Val	Ser	Val	Pro	Glu	Glu	Leu	Val	Gln	Ile	Gln	Ser	Tyr	
215								220				225				
TTG	AGG	TGG	GAG	AGG	AAG	GGA	AAA	CAG	AAT	TAC	CCC	CCT	GAG	AAA	GAG	836
Leu	Arg	Trp	Glu	Arg	Lys	Gly	Lys	Gln	Asn	Tyr	Pro	Pro	Glu	Lys	Glu	
230								235				240				
AAG	GAG	GAA	TAT	GAG	GCT	GCT	CGA	ACT	GTG	CTA	CAG	GAG	GAA	ATA	GCT	884
Lys	Glu	Glu	Tyr	Glu	Ala	Ala	Arg	Thr	Val	Leu	Gln	Glu	Glu	Ile	Ala	
245								250				255				
CGT	GGT	GCT	TCC	ATA	CAG	GAC	ATT	CGA	GCA	AGG	CTA	ACA	AAA	ACT	AAT	932
Arg	Gly	Ala	Ser	Ile	Gln	Asp	Ile	Arg	Ala	Arg	Leu	Thr	Lys	Thr	Asn	
265								270				275				

GAT AAA AGT CAA AGC AAA GAA GAG CCT CTT CAT GTA ACA AAG AGT GAT	980
Asp Lys Ser Gln Ser Lys Glu Glu Pro Leu His Val Thr Lys Ser Asp	
280 285 290	
ATA CCT GAT GAC CTT GCC CAA GCA CAA GCT TAC ATT AGG TGG GAG AAA	1028
Ile Pro Asp Asp Leu Ala Gln Ala Gln Ala Tyr Ile Arg Trp Glu Lys	
295 300 305	
GCA GGA AAG CCG AAC TAT CCT CCA GAA AAG CAA ATT GAA GAA CTC GAA	1076
Ala Gly Lys Pro Asn Tyr Pro Pro Glu Lys Gln Ile Glu Glu Leu Glu	
310 315 320	
GAA GCA AGA AGA GAA TTG CAA CTT GAG CTT GAG AAA GGC ATT ACC CTT	1124
Glu Ala Arg Arg Glu Leu Gln Leu Glu Leu Glu Lys Gly Ile Thr Leu	
325 330 335 340	
GAT GAG TTG CGG AAA ACG ATT ACA AAA GGG GAG ATA AAA ACT AAG GTG	1172
Asp Glu Leu Arg Lys Thr Ile Thr Lys Gly Glu Ile Lys Thr Lys Val	
345 350 355	
GAA AAG CAC CTG AAA AGA AGT TCT TTT GCC GTT GAA AGA ATC CAA AGA	1220
Glu Lys His Leu Lys Arg Ser Ser Phe Ala Val Glu Arg Ile Gln Arg	
360 365 370	
AAG AAG AGA GAC TTT GGG CAT CTT ATT AAT AAG TAT ACT TCC AGT CCT	1268
Lys Lys Arg Asp Phe Gly His Leu Ile Asn Lys Tyr Thr Ser Ser Pro	
375 380 385	
GCA GTA CAA GTA CAA AAG GTC TTG GAA GAA CCA CCA GCC TTA TCT AAA	1316
Ala Val Gln Val Gln Lys Val Leu Glu Glu Pro Pro Ala Leu Ser Lys	
390 395 400	
ATT AAG CTG TAT GCC AAG GAG AAG GAG GAG CAG ATT GAT GAT CCG ATC	1364
Ile Lys Leu Tyr Ala Lys Glu Lys Glu Glu Gln Ile Asp Asp Pro Ile	
405 410 415 420	
CTA AAT AAA AAG ATC TTT AAG GTC GAT GAT GGG GAG CTA CTG GTA CTG	1412
Leu Asn Lys Lys Ile Phe Lys Val Asp Asp Gly Glu Leu Leu Val Leu	
425 430 435	
GTA GCA AAG TCC TCT GGG AAG ACA AAA GTA CAT CTA GCT ACA GAT CTG	1460
Val Ala Lys Ser Ser Gly Lys Thr Lys Val His Leu Ala Thr Asp Leu	
440 445 450	
AAT CAG CCA ATT ACT CTT CAC TGG GCA TTA TCC AAA AGT CCT GGA GAG	1508
Asn Gln Pro Ile Thr Leu His Trp Ala Leu Ser Lys Ser Pro Gly Glu	
455 460 465	
TGG ATG GTA CCA CCT TCA AGC ATA TTG CCT CCT GGG TCA ATT ATT TTA	1556
Trp Met Val Pro Pro Ser Ser Ile Leu Pro Pro Gly Ser Ile Ile Leu	
470 475 480	
GAC AAG GCT GCC GAA ACA CCT TTT TCA GCC AGT TCT TCT GAT GGT CTA	1604
Asp Lys Ala Ala Glu Thr Pro Phe Ser Ala Ser Ser Ser Asp Gly Leu	
485 490 495 500	
ACT TCT AAG GTA CAA TCT TTG GAT ATA GTA ATT GAA GAT GGC AAT TTT	1652
Thr Ser Lys Val Gln Ser Leu Asp Ile Val Ile Glu Asp Gly Asn Phe	
505 510 515	

GTG GGG ATG CCA TTT GTT CTT TTG TCT GGT GAA AAA TGG ATT AAG AAC	1700
Val Gly Met Pro Phe Val Leu Leu Ser Gly Glu Lys Trp Ile Lys Asn	
520 525 530	
CAA GGG TCG GAT TTC TAT GTT GGC TTC AGT GCT GCA TCC AAA TTA GCA	1748
Gln Gly Ser Asp Phe Tyr Val Gly Phe Ser Ala Ala Ser Lys Leu Ala	
535 540 545	
CTC AAG GCT GCT GGG GAT GGC AGT GGA ACT GCA AAG TCT TTA CTG GAT	1796
Leu Lys Ala Ala Gly Asp Gly Ser Gly Thr Ala Lys Ser Leu Leu Asp	
550 555 560	
AAA ATA GCA GAT ATG GAA AGT GAG GCT CAG AAG TCA TTT ATG CAC CGG	1844
Lys Ile Ala Asp Met Glu Ser Glu Ala Gln Lys Ser Phe Met His Arg	
565 570 575 580	
TTT AAT ATT GCA GCT GAC TTG ATA GAA GAT GCC ACT AGT GCT GGT GAA	1892
Phe Asn Ile Ala Ala Asp Leu Ile Glu Asp Ala Thr Ser Ala Gly Glu	
585 590 595	
CTT GGT TTT GCT GGA ATT CTT GTA TGG ATG AGG TTC ATG GCT ACA AGG	1940
Leu Gly Phe Ala Gly Ile Leu Val Trp Met Arg Phe Met Ala Thr Arg	
600 605 610	
CAA CTG ATA TGG AAC AAA AAC TAT AAC GTA AAA CCA CGT GAA ATA AGC	1988
Gln Leu Ile Trp Asn Lys Asn Tyr Asn Val Lys Pro Arg Glu Ile Ser	
615 620 625	
AAG GCT CAG GAC AGA CTT ACA GAC TTG TTG CAG AAT GCT TTC ACC AGT	2036
Lys Ala Gln Asp Arg Leu Thr Asp Leu Leu Gln Asn Ala Phe Thr Ser	
630 635 640	
CAC CCT CAG TAC CGT GAA ATT TTG CGG ATG ATT ATG TCA ACT GTT GGA	2084
His Pro Gln Tyr Arg Glu Ile Leu Arg Met Ile Met Ser Thr Val Gly	
645 650 655 660	
CGT GGA GGT GAA GGG GAT GTA GGA CAG CGA ATT AGG GAT GAA ATT TTG	2132
Arg Gly Gly Glu Gly Asp Val Gly Gln Arg Ile Arg Asp Glu Ile Leu	
665 670 675	
GTC ATC CAG AGG AAC AAT GAC TGC AAG GGT GGT ATG ATG CAA GAA TGG	2180
Val Ile Gln Arg Asn Asn Asp Cys Lys Gly Gly Met Met Gln Glu Trp	
680 685 690	
CAT CAG AAA TTG CAT AAT AAT ACT AGT CCT GAT GAT GTT GTG ATC TGT	2228
His Gln Lys Leu His Asn Asn Thr Ser Pro Asp Asp Val Val Ile Cys	
695 700 705	
CAG GCA TTA ATT GAC TAC ATC AAG AGT GAT TTT GAT CTT GGT GTT TAT	2276
Gln Ala Leu Ile Asp Tyr Ile Lys Ser Asp Phe Asp Leu Gly Val Tyr	
710 715 720	
TGG AAA ACC CTG AAT GAG AAC GGA ATA ACA AAA GAG CGT CTT TTG AGT	2324
Trp Lys Thr Leu Asn Glu Asn Gly Ile Thr Lys Glu Arg Leu Leu Ser	
725 730 735 740	
TAT GAC CGT GCT ATC CAT TCT GAA CCA AAT TTT AGA GGA GAT CAA AAG	2372
Tyr Asp Arg Ala Ile His Ser Glu Pro Asn Phe Arg Gly Asp Gln Lys	
745 750 755	

GGT GGT CTT TTG CGT GAT TTA GGT CAC TAT ATG AGA ACA TTG AAG GCA	2420
Gly Gly Leu Leu Arg Asp Leu Gly His Tyr Met Arg Thr Leu Lys Ala	
760 765 770	
GTT CAT TCA GGT GCA GAT CTT GAG TCT GCT ATT GCA AAC TGC ATG GGC	2468
Val His Ser Gly Ala Asp Leu Glu Ser Ala Ile Ala Asn Cys Met Gly	
775 780 785	
TAC AAA ACT GAG GGA GAA GGC TTT ATG GTT GGA GTC CAG ATA AAT CCT	2516
Tyr Lys Thr Glu Gly Glu Gly Phe Met Val Gly Val Gln Ile Asn Pro	
790 795 800	
GTA TCA GGC TTG CCA TCT GGC TTT CAG GAC CTC CTC CAT TTT GTC TTA	2564
Val Ser Gly Leu Pro Ser Gly Phe Gln Asp Leu Leu His Phe Val Leu	
805 810 815 820	
GAC CAT GTG GAA GAT AAA AAT GTG GAA ACT CTT CTT GAG AGA TTG CTA	2612
Asp His Val Glu Asp Lys Asn Val Glu Thr Leu Leu Glu Arg Leu Leu	
825 830 835	
GAG GCT CGT GAG GAG CTT AGG CCC TTG CTT CTC AAA CCA AAC AAC CGT	2660
Glu Ala Arg Glu Glu Leu Arg Pro Leu Leu Leu Lys Pro Asn Asn Arg	
840 845 850	
CTA AAG GAT CTG CTG TTT TTG GAC ATA GCA CTT GAT TCT ACA GTT AGA	2708
Leu Lys Asp Leu Leu Phe Leu Asp Ile Ala Leu Asp Ser Thr Val Arg	
855 860 865	
ACA GCA GTA GAA AGG GGA TAT GAA GAA TTG AAC AAC GCT AAT CCT GAG	2756
Thr Ala Val Glu Arg Gly Tyr Glu Glu Leu Asn Asn Ala Asn Pro Glu	
870 875 880	
AAA ATC ATG TAC TTC ATC TCC CTC GTT CTT GAA AAT CTC GCA CTC TCT	2804
Lys Ile Met Tyr Phe Ile Ser Leu Val Leu Glu Asn Leu Ala Leu Ser	
885 890 895 900	
GTG GAC GAT AAT GAA GAT CTT GTT TAT TGC TTG AAG GGA TGG AAT CAA	2852
Val Asp Asp Asn Glu Asp Leu Val Tyr Cys Leu Lys Gly Trp Asn Gln	
905 910 915	
GCT CTT TCA ATG TCC AAT GGT GGG GAC AAC CAT TGG GCT TTA TTT GCA	2900
Ala Leu Ser Met Ser Asn Gly Gly Asp Asn His Trp Ala Leu Phe Ala	
920 925 930	
AAA GCT GTG CTT GAC AGA ACC CGT CTT GCA CTT GCA AGC AAG GCA GAG	2948
Lys Ala Val Leu Asp Arg Thr Arg Leu Ala Leu Ala Ser Lys Ala Glu	
935 940 945	
TGG TAC CAT CAC TTA TTG CAG CCA TCT GCC GAA TAT CTA GGA TCA ATA	2996
Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly Ser Ile	
950 955 960	
CTT GGG GTG GAC CAA TGG GCT TTG AAC ATA TTT ACT GAA GAA ATT ATA	3044
Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu Ile Ile	
965 970 975 980	
CGT GCT GGA TCA GCA GCT TCA TTA TCC TCT CTT CTT AAT AGA CTC GAT	3092
Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg Leu Asp	
985 990 995	

CCC GTG CTT CGG AAA ACT GCA AAT CTA GGA AGT TGG CAG ATT ATC AGT	3140
Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile Ile Ser	
1000 1005 1010	
CCA GTT GAA GCC GTT GGA TAT GTT GTC GTT GTG GAT GAG TTG CTT TCA	3188
Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp Glu Leu Leu Ser	
1015 1020 1025	
GTT CAG AAT GAA ATC TAC GAG AAG CCC ACG ATC TTA GTA GCA AAA TCT	3236
Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu Val Ala Lys Ser	
1030 1035 1040	
GTT AAA GGA GAG GAG GAA ATT CCT GAT GGT GCT GTT GCC CTG ATA ACA	3284
Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val Ala Leu Ile Thr	
1045 1050 1055 1060	
CCA GAC ATG CCA GAT GTT CTT TCA CAT GTT TCT GTT CGA GCT AGA AAT	3332
Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala Arg Asn	
1065 1070 1075	
GGG AAG GTT TGC TTT GCT ACA TGC TTT GAT CCC AAT ATA TTG GCT GAC	3380
Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn Ile Leu Ala Asp	
1080 1085 1090	
CTC CAA GCA AAG GAA GGA AGG ATT TTG CTC TTA AAG CCT ACA CCT TCA	3428
Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys Pro Thr Pro Ser	
1095 1100 1105	
GAC ATA ATC TAT AGT GAG GTG AAT GAG ATT GAG CTC CAA AGT TCA AGT	3476
Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser Ser Ser	
1110 1115 1120	
AAC TTG GTA GAA GCT GAA ACT TCA GCA ACA CTT AGA TTG GTG AAA AAG	3524
Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val Lys Lys	
1125 1130 1135 1140	
CAA TTT GGT GGT TGT TAC GCA ATA TCA GCA GAT GAA TTC ACA AGT GAA	3572
Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu Phe Thr Ser Glu	
1145 1150 1155	
ATG GTT GGA GCT AAA TCA CGT AAT ATT GCA TAT CTG AAA GGA AAA GTG	3620
Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu Lys Gly Lys Val	
1160 1165 1170	
CCT TCC TCG GTG GGA ATT CCT ACG TCA GTA GCT CTT CCA TTT GGA GTC	3668
Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu Pro Phe Gly Val	
1175 1180 1185	
TTT GAG AAA GTA CTT TCA GAC GAC ATA AAT CAG GGA GTG GCA AAA GAG	3716
Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly Val Ala Lys Glu	
1190 1195 1200	
TTG CAA ATT CTG ATG AAA AAA CTA TCT GAA GGA GAC TTC AGC GCT CTT	3764
Leu Gln Ile Leu Met Lys Lys Leu Ser Glu Gly Asp Phe Ser Ala Leu	
1205 1210 1215 1220	
GGT GAA ATT CGC ACA ACG GTT TTA GAT CTT TCA GCA CCA GCT CAA TTG	3812
Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Ala Pro Ala Gln Leu	
1225 1230 1235	

GTC AAA GAG CTG AAG GAG AAG ATG CAG GGT TCT GGC ATG CCT TGG CCT	3860
Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly Met Pro Trp Pro	
1240 1245 1250	
GGT GAT GAA GGT CCA AAG CGG TGG GAA CAA GCA TGG ATG GCC ATA AAA	3908
Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp Met Ala Ile Lys	
1255 1260 1265	
AAG GTG TGG GCT TCA AAA TGG AAT GAG AGA GCA TAC TTC AGC ACA AGG	3956
Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr Phe Ser Thr Arg	
1270 1275 1280	
AAG GTG AAA CTG GAT CAT GAC TAT CTG TGC ATG GCT GTC CTT GTT CAA	4004
Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala Val Leu Val Gln	
1285 1290 1295 1300	
GAA ATA ATA AAT GCT GAT TAT GCA TTT GTC ATT CAC ACA ACC AAC CCA	4052
Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His Thr Thr Asn Pro	
1305 1310 1315	
TCT TCC GGA GAC GAC TCA GAA ATA TAT GCC GAG GTG GTC AGG GGC CTT	4100
Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val Val Arg Gly Leu	
1320 1325 1330	
GGG GAA ACA CTT GTT GGA GCT TAT CCA GGA CGT GCT TTG AGT TTT ATC	4148
Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala Leu Ser Phe Ile	
1335 1340 1345	
TGC AAG AAA AAG GAT CTC AAC TCT CCT CAA GTG TTA GGT TAC CCA AGC	4196
Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu Gly Tyr Pro Ser	
1350 1355 1360	
AAA CCG ATC GGC CTT TTC ATA AAA AGA TCT ATC ATC TTC CGA TCT GAT	4244
Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile Phe Arg Ser Asp	
1365 1370 1375 1380	
TCC AAT GGG GAA GAT TTG GAA GGT TAT GCC GGT GCT GGC CTC TAC GAC	4292
Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala Gly Leu Tyr Asp	
1385 1390 1395	
AGT GTA CCA ATG GAT GAG GAG GAA AAA GTT GTA ATT GAT TAC TCT TCC	4340
Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile Asp Tyr Ser Ser	
1400 1405 1410	
GAC CCA TTG ATA ACT GAT GGT AAC TTC CGC CAG ACA ATC CTG TCC AAC	4388
Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr Ile Leu Ser Asn	
1415 1420 1425	
ATT GCT CGT GCT GGA CAT GCT ATC GAG GAG CTA TAT GGC TCT CCT CAA	4436
Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr Gly Ser Pro Gln	
1430 1435 1440	
GAC ATT GAG GGT GTA GTG AGG GAT GGA AAG ATT TAT GTC GTT CAG ACA	4484
Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr Val Val Gln Thr	
1445 1450 1455 1460	
AGA CCA CAG ATG T GATTATATTC TCGTTGTATG TTGTTTCAGAG AAGACCACAG	4537
Arg Pro Gln Met	

ATGTGATCAT ATTCTCATTG TATCAGATCT GTGACCACTT ACCTGATACC TCCCATGAAG 4597
 TTACCTGTAT GATTATACGT GATCCAAAGC CATCACATCA TGTTACCTT CAGCTATTGG 4657
 AGGAGAAGTG AGAAGTAGGA ATTGCAATAT GAGGAATAAT AAGAAAAACT TTGTAAAAGC 4717
 TAAATTAGCT GGGTATGATA TAGGGAGAAA TGTGTAAACA TTGTACTATA TATAGTATAT 4777
 ACACACGCAT TATGTATTGC ATTATGCACT GAATAATATC GCAGCATCAA AGAAGAAATC 4837
 CTTTGGGTGG TTTCAAAAA 4856

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1464 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ser Asn Ser Leu Gly Asn Asn Leu Leu Tyr Gln Gly Phe Leu Thr
 1 5 10 15
 Ser Thr Val Leu Glu His Lys Ser Arg Ile Ser Pro Pro Cys Val Gly
 20 25 30
 Gly Asn Ser Leu Phe Gln Gln Gln Val Ile Ser Lys Ser Pro Leu Ser
 35 40 45
 Thr Glu Phe Arg Gly Asn Arg Leu Lys Val Gln Lys Lys Lys Ile Pro
 50 55 60
 Met Glu Lys Lys Arg Ala Phe Ser Ser Ser Pro His Ala Val Leu Thr
 65 70 75 80
 Thr Asp Thr Ser Ser Glu Leu Ala Glu Lys Phe Ser Leu Gly Gly Asn
 85 90 95
 Ile Glu Leu Gln Val Asp Val Arg Pro Pro Thr Ser Gly Asp Val Ser
 100 105 110
 Phe Val Asp Phe Gln Val Thr Asn Gly Ser Asp Lys Leu Phe Leu His
 115 120 125
 Trp Gly Ala Val Lys Phe Gly Lys Glu Thr Trp Ser Leu Pro Asn Asp
 130 135 140
 Arg Pro Asp Gly Thr Lys Val Tyr Lys Asn Lys Ala Leu Arg Thr Pro
 145 150 155 160
 Phe Val Lys Ser Gly Ser Asn Ser Ile Leu Arg Leu Glu Ile Arg Asp
 165 170 175
 Thr Ala Ile Glu Ala Ile Glu Phe Leu Ile Tyr Asp Glu Ala His Asp
 180 185 190

Lys Trp Ile Lys Asn Asn Gly Gly Asn Phe Arg Val Lys Leu Ser Arg
 195 200 205
 Lys Glu Ile Arg Gly Pro Asp Val Ser Val Pro Glu Glu Leu Val Gln
 210 215 220
 Ile Gln Ser Tyr Leu Arg Trp Glu Arg Lys Gly Lys Gln Asn Tyr Pro
 225 230 235 240
 Pro Glu Lys Glu Lys Glu Glu Tyr Glu Ala Ala Arg Thr Val Leu Gln
 245 250 255
 Glu Glu Ile Ala Arg Gly Ala Ser Ile Gln Asp Ile Arg Ala Arg Leu
 260 265 270
 Thr Lys Thr Asn Asp Lys Ser Gln Ser Lys Glu Glu Pro Leu His Val
 275 280 285
 Thr Lys Ser Asp Ile Pro Asp Asp Leu Ala Gln Ala Gln Ala Tyr Ile
 290 295 300
 Arg Trp Glu Lys Ala Gly Lys Pro Asn Tyr Pro Pro Glu Lys Gln Ile
 305 310 315 320
 Glu Glu Leu Glu Glu Ala Arg Arg Glu Leu Gln Leu Glu Leu Glu Lys
 325 330 335
 Gly Ile Thr Leu Asp Glu Leu Arg Lys Thr Ile Thr Lys Gly Glu Ile
 340 345 350
 Lys Thr Lys Val Glu Lys His Leu Lys Arg Ser Ser Phe Ala Val Glu
 355 360 365
 Arg Ile Gln Arg Lys Lys Arg Asp Phe Gly His Leu Ile Asn Lys Tyr
 370 375 380
 Thr Ser Ser Pro Ala Val Gln Val Gln Lys Val Leu Glu Glu Pro Pro
 385 390 395 400
 Ala Leu Ser Lys Ile Lys Leu Tyr Ala Lys Glu Lys Glu Glu Gln Ile
 405 410 415
 Asp Asp Pro Ile Leu Asn Lys Lys Ile Phe Lys Val Asp Asp Gly Glu
 420 425 430
 Leu Leu Val Leu Val Ala Lys Ser Ser Gly Lys Thr Lys Val His Leu
 435 440 445
 Ala Thr Asp Leu Asn Gln Pro Ile Thr Leu His Trp Ala Leu Ser Lys
 450 455 460
 Ser Pro Gly Glu Trp Met Val Pro Pro Ser Ser Ile Leu Pro Pro Gly
 465 470 475 480
 Ser Ile Ile Leu Asp Lys Ala Ala Glu Thr Pro Phe Ser Ala Ser Ser
 485 490 495
 Ser Asp Gly Leu Thr Ser Lys Val Gln Ser Leu Asp Ile Val Ile Glu
 500 505 510

Asp	Gly	Asn	Phe	Val	Gly	Met	Pro	Phe	Val	Leu	Leu	Ser	Gly	Glu	Lys	515	520	525
Trp	Ile	Lys	Asn	Gln	Gly	Ser	Asp	Phe	Tyr	Val	Gly	Phe	Ser	Ala	Ala	530	535	540
Ser	Lys	Leu	Ala	Leu	Lys	Ala	Ala	Gly	Asp	Gly	Ser	Gly	Thr	Ala	Lys	545	550	555
Ser	Leu	Leu	Asp	Lys	Ile	Ala	Asp	Met	Glu	Ser	Glu	Ala	Gln	Lys	Ser	565	570	575
Phe	Met	His	Arg	Phe	Asn	Ile	Ala	Ala	Asp	Leu	Ile	Glu	Asp	Ala	Thr	580	585	590
Ser	Ala	Gly	Glu	Leu	Gly	Phe	Ala	Gly	Ile	Leu	Val	Trp	Met	Arg	Phe	595	600	605
Met	Ala	Thr	Arg	Gln	Leu	Ile	Trp	Asn	Lys	Asn	Tyr	Asn	Val	Lys	Pro	610	615	620
Arg	Glu	Ile	Ser	Lys	Ala	Gln	Asp	Arg	Leu	Thr	Asp	Leu	Leu	Gln	Asn	625	630	635
Ala	Phe	Thr	Ser	His	Pro	Gln	Tyr	Arg	Glu	Ile	Leu	Arg	Met	Ile	Met	645	650	655
Ser	Thr	Val	Gly	Arg	Gly	Gly	Glu	Gly	Asp	Val	Gly	Gln	Arg	Ile	Arg	660	665	670
Asp	Glu	Ile	Leu	Val	Ile	Gln	Arg	Asn	Asn	Asp	Cys	Lys	Gly	Gly	Met	675	680	685
Met	Gln	Glu	Trp	His	Gln	Lys	Leu	His	Asn	Asn	Thr	Ser	Pro	Asp	Asp	690	695	700
Val	Val	Ile	Cys	Gln	Ala	Leu	Ile	Asp	Tyr	Ile	Lys	Ser	Asp	Phe	Asp	705	710	715
Leu	Gly	Val	Tyr	Trp	Lys	Thr	Leu	Asn	Glu	Asn	Gly	Ile	Thr	Lys	Glu	725	730	735
Arg	Leu	Leu	Ser	Tyr	Asp	Arg	Ala	Ile	His	Ser	Glu	Pro	Asn	Phe	Arg	740	745	750
Gly	Asp	Gln	Lys	Gly	Gly	Leu	Leu	Arg	Asp	Leu	Gly	His	Tyr	Met	Arg	755	760	765
Thr	Leu	Lys	Ala	Val	His	Ser	Gly	Ala	Asp	Leu	Glu	Ser	Ala	Ile	Ala	770	775	780
Asn	Cys	Met	Gly	Tyr	Lys	Thr	Glu	Gly	Glu	Gly	Phe	Met	Val	Gly	Val	785	790	795
Gln	Ile	Asn	Pro	Val	Ser	Gly	Leu	Pro	Ser	Gly	Phe	Gln	Asp	Leu	Leu	805	810	815
His	Phe	Val	Leu	Asp	His	Val	Glu	Asp	Lys	Asn	Val	Glu	Thr	Leu	Leu	820	825	830

Glu Arg Leu Leu Glu Ala Arg Glu Glu Leu Arg Pro Leu Leu Leu Lys	835	840	845
Pro Asn Asn Arg Leu Lys Asp Leu Leu Phe Leu Asp Ile Ala Leu Asp	850	855	860
Ser Thr Val Arg Thr Ala Val Glu Arg Gly Tyr Glu Glu Leu Asn Asn	865	870	875 880
Ala Asn Pro Glu Lys Ile Met Tyr Phe Ile Ser Leu Val Leu Glu Asn	885	890	895
Leu Ala Leu Ser Val Asp Asp Asn Glu Asp Leu Val Tyr Cys Leu Lys	900	905	910
Gly Trp Asn Gln Ala Leu Ser Met Ser Asn Gly Gly Asp Asn His Trp	915	920	925
Ala Leu Phe Ala Lys Ala Val Leu Asp Arg Thr Arg Leu Ala Leu Ala	930	935	940
Ser Lys Ala Glu Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr	945	950	955 960
Leu Gly Ser Ile Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr	965	970	975
Glu Glu Ile Ile Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu	980	985	990
Asn Arg Leu Asp Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp	995	1000	1005
Gln Ile Ile Ser Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp	1010	1015	1020
Glu Leu Leu Ser Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu	1025	1030	1035 1040
Val Ala Lys Ser Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val	1045	1050	1055
Ala Leu Ile Thr Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val	1060	1065	1070
Arg Ala Arg Asn Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn	1075	1080	1085
Ile Leu Ala Asp Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys	1090	1095	1100
Pro Thr Pro Ser Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu	1105	1110	1115 1120
Gln Ser Ser Ser Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg	1125	1130	1135
Leu Val Lys Lys Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu	1140	1145	1150

Phe Thr Ser Glu Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu
 1155 1160 1165
 Lys Gly Lys Val Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu
 1170 1175 1180
 Pro Phe Gly Val Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly
 1185 1190 1195 1200
 Val Ala Lys Glu Leu Gln Ile Leu Met Lys Lys Leu Ser Glu Gly Asp
 1205 1210 1215
 Phe Ser Ala Leu Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Ala
 1220 1225 1230
 Pro Ala Gln Leu Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly
 1235 1240 1245
 Met Pro Trp Pro Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp
 1250 1255 1260
 Met Ala Ile Lys Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr
 1265 1270 1275 1280
 Phe Ser Thr Arg Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala
 1285 1290 1295
 Val Leu Val Gln Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His
 1300 1305 1310
 Thr Thr Asn Pro Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val
 1315 1320 1325
 Val Arg Gly Leu Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala
 1330 1335 1340
 Leu Ser Phe Ile Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu
 1345 1350 1355 1360
 Gly Tyr Pro Ser Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile
 1365 1370 1375
 Phe Arg Ser Asp Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala
 1380 1385 1390
 Gly Leu Tyr Asp Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile
 1395 1400 1405
 Asp Tyr Ser Ser Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr
 1410 1415 1420
 Ile Leu Ser Asn Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr
 1425 1430 1435 1440
 Gly Ser Pro Gln Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr
 1445 1450 1455
 Val Val Gln Thr Arg Pro Gln Met
 1460

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1918 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Solanum tuberosum*
- (B) STRAIN: C.V. Desiree

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..1555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCA GAG TGG TAC CAT CAC TTA TTG CAG CCA TCT GCC GAA TAT CTA GGA	48
Ala Glu Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly	
1 5 10 15	
TCA ATA CTT GGG GTG GAC CAA TGG GCT TTG AAC ATA TTT ACT GAA GAA	96
Ser Ile Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu	
20 25 30	
ATT ATA CGT GCT GGA TCA GCA GCT TCA TTA TCC TCT CTT CTT AAT AGA	144
Ile Ile Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg	
35 40 45	
CTC GAT CCC GTG CTT CGG AAA ACT GCA AAT CTA GGA AGT TGG CAG ATT	192
Leu Asp Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile	
50 55 60	
ATC AGT CCA GTT GAA GCC GTT GGA TAT GTT GTC GTT GTG GAT GAG TTG	240
Ile Ser Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp Glu Leu	
65 70 75 80	
CTT TCA GTT CAG AAT GAA ATC TAC GAG AAG CCC ACG ATC TTA GTA GCA	288
Leu Ser Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu Val Ala	
85 90 95	
AAA TCT GTT AAA GGA GAG GAG GAA ATT CCT GAT GGT GCT GTT GCC CTG	336
Lys Ser Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val Ala Leu	
100 105 110	
ATA ACA CCA GAC ATG CCA GAT GTT CTT TCA CAT GTT TCT GTT CGA GCT	384
Ile Thr Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala	
115 120 125	
AGA AAT GGG AAG GTT TGC TTT GCT ACA TGC TTT GAT CCC AAT ATA TTG	432
Arg Asn Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn Ile Leu	
130 135 140	
GCT GAC CTC CAA GCA AAG GAA GGA AGG ATT TTG CTC TTA AAG CCT ACA	480
Ala Asp Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys Pro Thr	
145 150 155 160	

CCT TCA GAC ATA ATC TAT AGT GAG GTG AAT GAG ATT GAG CTC CAA AGT	528
Pro Ser Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser	
165 170 175	
TCA AGT AAC TTG GTA GAA GCT GAA ACT TCA GCA ACA CTT AGA TTG GTG	576
Ser Ser Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val	
180 185 190	
AAA AAG CAA TTT GGT GGT TGT TAC GCA ATA TCA GCA GAT GAA TTC ACA	624
Lys Lys Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu Phe Thr	
195 200 205	
AGT GAA ATG GTT GGA GCT AAA TCA CGT AAT ATT GCA TAT CTG AAA GGA	672
Ser Glu Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu Lys Gly	
210 215 220	
AAA GTG CCT TCC TCG GTG GGA ATT CCT ACG TCA GTA GCT CTT CCA TTT	720
Lys Val Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu Pro Phe	
225 230 235 240	
GGA GTC TTT GAG AAA GTA CTT TCA GAC GAC ATA AAT CAG GGA GTG GCA	768
Gly Val Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly Val Ala	
245 250 255	
AAA GAG TTG CAA ATT CTG ACA AAA AAA CTA TCT GAA GGA GAC TTT AGC	816
Lys Glu Leu Gln Ile Leu Thr Lys Lys Leu Ser Glu Gly Asp Phe Ser	
260 265 270	
GCT CTT GGT GAA ATT CGC ACA ACG GTT TTA GAT CTT TCG ACA CCA GCT	864
Ala Leu Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Thr Pro Ala	
275 280 285	
CAA TTG GTC AAA GAG CTG AAG GAG AAG ATG CAG GGT TCT GGC ATG CCT	912
Gln Leu Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly Met Pro	
290 295 300	
TGG CCT GGT GAT GAA GGT CCA AAG CGG TGG GAA CAA GCA TGG ATG GCC	960
Trp Pro Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp Met Ala	
305 310 315 320	
ATA AAA AAG GTG TGG GCT TCA AAA TGG AAT GAG AGA GCA TAC TTC AGC	1008
Ile Lys Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr Phe Ser	
325 330 335	
ACA AGG AAG GTG AAA CTG GAT CAT GAC TAT CTG TGC ATG GCT GTC CTT	1056
Thr Arg Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala Val Leu	
340 345 350	
GTT CAA GAA ATA ATA AAT GCT GAT TAT GCA TTT GTC ATT CAC ACA ACC	1104
Val Gln Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His Thr Thr	
355 360 365	
AAC CCA TCT TCC GGA GAC GAC TCA GAA ATA TAT GCC GAG GTG GTC AGG	1152
Asn Pro Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val Val Arg	
370 375 380	
GGC CTT GGG GAA ACA CTT GTT GGA GCT TAT CCA GGA CGT GCT TTG AGT	1200
Gly Leu Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala Leu Ser	
385 390 395 400	

TTT ATC TGC AAG AAA AAG GAT CTC AAC TCT CCT CAA GTG TTA GGT TAC	1248
Phe Ile Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu Gly Tyr	
405 410 415	
CCA AGC AAA CCG ATC GGC CTT TTC ATA AAA AGA TCT ATC ATC TTC CGA	1296
Pro Ser Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile Phe Arg	
420 425 430	
TCT GAT TCC AAT GGG GAA GAT TTG GAA GGT TAT GCC GGT GCT GGC CTC	1344
Ser Asp Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala Gly Leu	
435 440 445	
TAC GAC AGT GTA CCA ATG GAT GAG GAG GAA AAA GTT GTA ATT GAT TAC	1392
Tyr Asp Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile Asp Tyr	
450 455 460	
TCT TCC GAC CCA TTG ATA ACT GAT GGT AAC TTC CGC CAG ACA ATC CTG	1440
Ser Ser Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr Ile Leu	
465 470 475 480	
TCC AAC ATT GCT CGT GCT GGA CAT GCT ATC GAG GAG CTA TAT GGC TCT	1488
Ser Asn Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr Gly Ser	
485 490 495	
CCT CAA GAC ATT GAG GGT GTA GTG AGG GAT GGA AAG ATT TAT GTC GTT	1536
Pro Gln Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr Val Val	
500 505 510	
CAG ACA AGA CCA CAG ATG T GATTATATTC TCGTTGTATG TTGTTTCAGAG	1585
Gln Thr Arg Pro Gln Met	
515	
AAGACCACAG ATGTGATCAT ATTCTCATTG TATCAGATCT GTGACCACTT ACCTGATACC	1645
TCCCATGAAG TTACCTGTAT GATTATACGT GATCCAAAGC CATCACATCA TGTTACCTT	1705
CAGCTATTGG AGGAGAAGTG AGAAGTAGGA ATTGCAATAT GAGGAATAAT AAGAAAAACT	1765
TTGTAAAAGC TAAATTAGCT GGGTATGATA TAGGGAGAAA TGTGTAAACA TTGTACTATA	1825
TATAGTATAT ACACACGCAT TATGTATTGC ATTATGCACT GAATAATATC GCAGCATCAA	1885
AGAAGAAATC CTTTGGGTGG TTTCAAAAAA AAA	1918

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Ala Glu Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly	
1 5 10 15	
Ser Ile Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu	
20 25 30	

Ile	Ile	Arg	Ala	Gly	Ser	Ala	Ala	Ser	Leu	Ser	Ser	Leu	Leu	Asn	Arg
35						40						45			
Leu	Asp	Pro	Val	Leu	Arg	Lys	Thr	Ala	Asn	Leu	Gly	Ser	Trp	Gln	Ile
50						55				60					
Ile	Ser	Pro	Val	Glu	Ala	Val	Gly	Tyr	Val	Val	Val	Val	Asp	Glu	Leu
65				70						75				80	
Leu	Ser	Val	Gln	Asn	Glu	Ile	Tyr	Glu	Lys	Pro	Thr	Ile	Leu	Val	Ala
				85				90						95	
Lys	Ser	Val	Lys	Gly	Glu	Glu	Glu	Ile	Pro	Asp	Gly	Ala	Val	Ala	Leu
		100						105				110			
Ile	Thr	Pro	Asp	Met	Pro	Asp	Val	Leu	Ser	His	Val	Ser	Val	Arg	Ala
		115				120						125			
Arg	Asn	Gly	Lys	Val	Cys	Phe	Ala	Thr	Cys	Phe	Asp	Pro	Asn	Ile	Leu
130						135				140					
Ala	Asp	Leu	Gln	Ala	Lys	Glu	Gly	Arg	Ile	Leu	Leu	Leu	Lys	Pro	Thr
145				150						155				160	
Pro	Ser	Asp	Ile	Ile	Tyr	Ser	Glu	Val	Asn	Glu	Ile	Glu	Leu	Gln	Ser
				165				170						175	
Ser	Ser	Asn	Leu	Val	Glu	Ala	Glu	Thr	Ser	Ala	Thr	Leu	Arg	Leu	Val
		180						185				190			
Lys	Lys	Gln	Phe	Gly	Gly	Cys	Tyr	Ala	Ile	Ser	Ala	Asp	Glu	Phe	Thr
195						200						205			
Ser	Glu	Met	Val	Gly	Ala	Lys	Ser	Arg	Asn	Ile	Ala	Tyr	Leu	Lys	Gly
210						215				220					
Lys	Val	Pro	Ser	Ser	Val	Gly	Ile	Pro	Thr	Ser	Val	Ala	Leu	Pro	Phe
225				230						235				240	
Gly	Val	Phe	Glu	Lys	Val	Leu	Ser	Asp	Asp	Ile	Asn	Gln	Gly	Val	Ala
				245				250						255	
Lys	Glu	Leu	Gln	Ile	Leu	Thr	Lys	Lys	Leu	Ser	Glu	Gly	Asp	Phe	Ser
		260						265				270			
Ala	Leu	Gly	Glu	Ile	Arg	Thr	Thr	Val	Leu	Asp	Leu	Ser	Thr	Pro	Ala
		275				280						285			
Gln	Leu	Val	Lys	Glu	Leu	Lys	Glu	Lys	Met	Gln	Gly	Ser	Gly	Met	Pro
290						295				300					
Trp	Pro	Gly	Asp	Glu	Gly	Pro	Lys	Arg	Trp	Glu	Gln	Ala	Trp	Met	Ala
305				310						315				320	
Ile	Lys	Lys	Val	Trp	Ala	Ser	Lys	Trp	Asn	Glu	Arg	Ala	Tyr	Phe	Ser
				325				330						335	
Thr	Arg	Lys	Val	Lys	Leu	Asp	His	Asp	Tyr	Leu	Cys	Met	Ala	Val	Leu
		340						345				350			

Val	Gln	Glu	Ile	Ile	Asn	Ala	Asp	Tyr	Ala	Phe	Val	Ile	His	Thr	Thr	
		355					360					365				
Asn	Pro	Ser	Ser	Gly	Asp	Asp	Ser	Glu	Ile	Tyr	Ala	Glu	Val	Val	Arg	
	370					375					380					
Gly	Leu	Gly	Glu	Thr	Leu	Val	Gly	Ala	Tyr	Pro	Gly	Arg	Ala	Leu	Ser	
385					390					395					400	
Phe	Ile	Cys	Lys	Lys	Lys	Asp	Leu	Asn	Ser	Pro	Gln	Val	Leu	Gly	Tyr	
				405					410					415		
Pro	Ser	Lys	Pro	Ile	Gly	Leu	Phe	Ile	Lys	Arg	Ser	Ile	Ile	Phe	Arg	
			420					425					430			
Ser	Asp	Ser	Asn	Gly	Glu	Asp	Leu	Glu	Gly	Tyr	Ala	Gly	Ala	Gly	Leu	
		435					440					445				
Tyr	Asp	Ser	Val	Pro	Met	Asp	Glu	Glu	Glu	Lys	Val	Val	Ile	Asp	Tyr	
	450					455					460					
Ser	Ser	Asp	Pro	Leu	Ile	Thr	Asp	Gly	Asn	Phe	Arg	Gln	Thr	Ile	Leu	
465					470					475					480	
Ser	Asn	Ile	Ala	Arg	Ala	Gly	His	Ala	Ile	Glu	Glu	Leu	Tyr	Gly	Ser	
				485					490					495		
Pro	Gln	Asp	Ile	Glu	Gly	Val	Val	Arg	Asp	Gly	Lys	Ile	Tyr	Val	Val	
			500					505					510			
Gln	Thr	Arg	Pro	Gln	Met											
			515													

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Jens Kossmann
Ruth Lorberth
- (ii) TITLE OF INVENTION: PLANTS WHICH SYNTHESIZE A MODIFIED STARCH,
PROCESS FOR THE PRODUCTION THEREOF AND MODIFIED STARCH
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: FISH & NEAVE
 - (B) STREET: 1251 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: USA
 - (F) ZIP: 10020
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) Classification:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/EP96/04109
 - (B) FILING DATE: 19-SEP-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: DE 19547733.2
 - (B) FILING DATE: 20-DEC-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: DE 19534759.5
 - (B) FILING DATE: 19-SEP-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Haley Jr., James F.
 - (B) REGISTRATION NUMBER: 27,794
 - (C) REFERENCE/DOCKET NUMBER: GFB-5
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 212-596-9000
 - (B) TELEFAX: 212-596-9090

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4856 base pairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Solanum tuberosum
 (B) STRAIN: C.V. Berolina

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION:105..4497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CATCTTCATC GAATTTCTCG AAGCTTCTTC GCTAATTTCC TGGTTTCTTC ACTCAAAATC	60
GACGTTTCTA GCTGAACTTG AGTGAATTAA GCCAGTGGGA GGAT ATG AGT AAT TCC	116
Met Ser Asn Ser	
1	
TTA GGG AAT AAC TTG CTG TAC CAG GGA TTC CTA ACC TCA ACA GTG TTG	164
Leu Gly Asn Asn Leu Leu Tyr Gln Gly Phe Leu Thr Ser Thr Val Leu	
5 10 15 20	
GAA CAT AAA AGT AGA ATC AGT CCT CCT TGT GTT GGA GGC AAT TCT TTG	212
Glu His Lys Ser Arg Ile Ser Pro Pro Cys Val Gly Gly Asn Ser Leu	
25 30 35	
TTT CAA CAA CAA GTG ATC TCG AAA TCA CCT TTA TCA ACT GAG TTT CGA	260
Phe Gln Gln Gln Val Ile Ser Lys Ser Pro Leu Ser Thr Glu Phe Arg	
40 45 50	
GGT AAC AGG TTA AAG GTG CAG AAA AAG AAA ATA CCT ATG GAA AAG AAG	308
Gly Asn Arg Leu Lys Val Gln Lys Lys Lys Ile Pro Met Glu Lys Lys	
55 60 65	
CGT GCT TTT TCT AGT TCT CCT CAT GCT GTA CTT ACC ACT GAT ACC TCT	356
Arg Ala Phe Ser Ser Ser Pro His Ala Val Leu Thr Thr Asp Thr Ser	
70 75 80	
TCT GAG CTA GCA GAA AAG TTC AGT CTA GGG GGG AAT ATT GAG CTA CAG	404
Ser Glu Leu Ala Glu Lys Phe Ser Leu Gly Gly Asn Ile Glu Leu Gln	
85 90 95 100	
GTT GAT GTT AGG CCT CCC ACT TCA GGT GAT GTG TCC TTT GTG GAT TTT	452
Val Asp Val Arg Pro Pro Thr Ser Gly Asp Val Ser Phe Val Asp Phe	
105 110 115	
CAA GTA ACA AAT GGT AGT GAT AAA CTG TTT TTG CAC TGG GGG GCA GTA	500
Gln Val Thr Asn Gly Ser Asp Lys Leu Phe Leu His Trp Gly Ala Val	
120 125 130	
AAA TTC GGG AAA GAA ACA TGG TCT CTT CCG AAT GAT CGT CCA GAT GGG	548
Lys Phe Gly Lys Glu Thr Trp Ser Leu Pro Asn Asp Arg Pro Asp Gly	
135 140 145	
ACC AAA GTG TAC AAG AAC AAA GCA CTT AGA ACT CCA TTT GTT AAA TCT	596
Thr Lys Val Tyr Lys Asn Lys Ala Leu Arg Thr Pro Phe Val Lys Ser	
150 155 160	
GGC TCT AAC TCC ATC CTG AGA CTG GAG ATA CGA GAC ACT GCT ATC GAA	644
Gly Ser Asn Ser Ile Leu Arg Leu Glu Ile Arg Asp Thr Ala Ile Glu	
165 170 175 180	
GCT ATT GAG TTT CTC ATA TAC GAT GAA GCC CAC GAT AAA TGG ATA AAG	692
Ala Ile Glu Phe Leu Ile Tyr Asp Glu Ala His Asp Lys Trp Ile Lys	
185 190 195	

AAT AAT GGT GGT AAT TTT CGT GTC AAA TTG TCA AGA AAA GAG ATA CGA	740
Asn Asn Gly Gly Asn Phe Arg Val Lys Leu Ser Arg Lys Glu Ile Arg	
200 205 210	
GGC CCA GAT GTT TCT GTT CCT GAG GAG CTT GTA CAG ATC CAA TCA TAT	788
Gly Pro Asp Val Ser Val Pro Glu Glu Leu Val Gln Ile Gln Ser Tyr	
215 220 225	
TTG AGG TGG GAG AGG AAG GGA AAA CAG AAT TAC CCC CCT GAG AAA GAG	836
Leu Arg Trp Glu Arg Lys Gly Lys Gln Asn Tyr Pro Pro Glu Lys Glu	
230 235 240	
AAG GAG GAA TAT GAG GCT GCT CGA ACT GTG CTA CAG GAG GAA ATA GCT	884
Lys Glu Glu Tyr Glu Ala Ala Arg Thr Val Leu Gln Glu Glu Ile Ala	
245 250 255 260	
CGT GGT GCT TCC ATA CAG GAC ATT CGA GCA AGG CTA ACA AAA ACT AAT	932
Arg Gly Ala Ser Ile Gln Asp Ile Arg Ala Arg Leu Thr Lys Thr Asn	
265 270 275	
GAT AAA AGT CAA AGC AAA GAA GAG CCT CTT CAT GTA ACA AAG AGT GAT	980
Asp Lys Ser Gln Ser Lys Glu Glu Pro Leu His Val Thr Lys Ser Asp	
280 285 290	
ATA CCT GAT GAC CTT GCC CAA GCA CAA GCT TAC ATT AGG TGG GAG AAA	1028
Ile Pro Asp Asp Leu Ala Gln Ala Gln Ala Tyr Ile Arg Trp Glu Lys	
295 300 305	
GCA GGA AAG CCG AAC TAT CCT CCA GAA AAG CAA ATT GAA GAA CTC GAA	1076
Ala Gly Lys Pro Asn Tyr Pro Pro Glu Lys Gln Ile Glu Glu Leu Glu	
310 315 320	
GAA GCA AGA AGA GAA TTG CAA CTT GAG CTT GAG AAA GGC ATT ACC CTT	1124
Glu Ala Arg Arg Glu Leu Gln Leu Glu Leu Glu Lys Gly Ile Thr Leu	
325 330 335 340	
GAT GAG TTG CGG AAA ACG ATT ACA AAA GGG GAG ATA AAA ACT AAG GTG	1172
Asp Glu Leu Arg Lys Thr Ile Thr Lys Gly Glu Ile Lys Thr Lys Val	
345 350 355	
GAA AAG CAC CTG AAA AGA AGT TCT TTT GCC GTT GAA AGA ATC CAA AGA	1220
Glu Lys His Leu Lys Arg Ser Ser Phe Ala Val Glu Arg Ile Gln Arg	
360 365 370	
AAG AAG AGA GAC TTT GGG CAT CTT ATT AAT AAG TAT ACT TCC AGT CCT	1268
Lys Lys Arg Asp Phe Gly His Leu Ile Asn Lys Tyr Thr Ser Ser Pro	
375 380 385	
GCA GTA CAA GTA CAA AAG GTC TTG GAA GAA CCA CCA GCC TTA TCT AAA	1316
Ala Val Gln Val Gln Lys Val Leu Glu Glu Pro Pro Ala Leu Ser Lys	
390 395 400	
ATT AAG CTG TAT GCC AAG GAG AAG GAG GAG CAG ATT GAT GAT CCG ATC	1364
Ile Lys Leu Tyr Ala Lys Glu Lys Glu Glu Gln Ile Asp Asp Pro Ile	
405 410 415 420	
CTA AAT AAA AAG ATC TTT AAG GTC GAT GAT GGG GAG CTA CTG GTA CTG	1412
Leu Asn Lys Lys Ile Phe Lys Val Asp Asp Gly Glu Leu Leu Val Leu	
425 430 435	
GTA GCA AAG TCC TCT GGG AAG ACA AAA GTA CAT CTA GCT ACA GAT CTG	1460
Val Ala Lys Ser Ser Gly Lys Thr Lys Val His Leu Ala Thr Asp Leu	
440 445 450	

AAT CAG CCA ATT ACT CTT CAC TGG GCA TTA TCC AAA AGT CCT GGA GAG	1508
Asn Gln Pro Ile Thr Leu His Trp Ala Leu Ser Lys Ser Pro Gly Glu	
455 460 465	
TGG ATG GTA CCA CCT TCA AGC ATA TTG CCT CCT GGG TCA ATT ATT TTA	1556
Trp Met Val Pro Pro Ser Ser Ile Leu Pro Pro Gly Ser Ile Ile Leu	
470 475 480	
GAC AAG GCT GCC GAA ACA CCT TTT TCA GCC AGT TCT TCT GAT GGT CTA	1604
Asp Lys Ala Ala Glu Thr Pro Phe Ser Ala Ser Ser Ser Asp Gly Leu	
485 490 495 500	
ACT TCT AAG GTA CAA TCT TTG GAT ATA GTA ATT GAA GAT GGC AAT TTT	1652
Thr Ser Lys Val Gln Ser Leu Asp Ile Val Ile Glu Asp Gly Asn Phe	
505 510 515	
GTG GGG ATG CCA TTT GTT CTT TTG TCT GGT GAA AAA TGG ATT AAG AAC	1700
Val Gly Met Pro Phe Val Leu Leu Ser Gly Glu Lys Trp Ile Lys Asn	
520 525 530	
CAA GGG TCG GAT TTC TAT GTT GGC TTC AGT GCT GCA TCC AAA TTA GCA	1748
Gln Gly Ser Asp Phe Tyr Val Gly Phe Ser Ala Ala Ser Lys Leu Ala	
535 540 545	
CTC AAG GCT GCT GGG GAT GGC AGT GGA ACT GCA AAG TCT TTA CTG GAT	1796
Leu Lys Ala Ala Gly Asp Gly Ser Gly Thr Ala Lys Ser Leu Leu Asp	
550 555 560	
AAA ATA GCA GAT ATG GAA AGT GAG GCT CAG AAG TCA TTT ATG CAC CGG	1844
Lys Ile Ala Asp Met Glu Ser Glu Ala Gln Lys Ser Phe Met His Arg	
565 570 575 580	
TTT AAT ATT GCA GCT GAC TTG ATA GAA GAT GCC ACT AGT GCT GGT GAA	1892
Phe Asn Ile Ala Ala Asp Leu Ile Glu Asp Ala Thr Ser Ala Gly Glu	
585 590 595	
CTT GGT TTT GCT GGA ATT CTT GTA TGG ATG AGG TTC ATG GCT ACA AGG	1940
Leu Gly Phe Ala Gly Ile Leu Val Trp Met Arg Phe Met Ala Thr Arg	
600 605 610	
CAA CTG ATA TGG AAC AAA AAC TAT AAC GTA AAA CCA CGT GAA ATA AGC	1988
Gln Leu Ile Trp Asn Lys Asn Tyr Asn Val Lys Pro Arg Glu Ile Ser	
615 620 625	
AAG GCT CAG GAC AGA CTT ACA GAC TTG TTG CAG AAT GCT TTC ACC AGT	2036
Lys Ala Gln Asp Arg Leu Thr Asp Leu Leu Gln Asn Ala Phe Thr Ser	
630 635 640	
CAC CCT CAG TAC CGT GAA ATT TTG CGG ATG ATT ATG TCA ACT GTT GGA	2084
His Pro Gln Tyr Arg Glu Ile Leu Arg Met Ile Met Ser Thr Val Gly	
645 650 655 660	
CGT GGA GGT GAA GGG GAT GTA GGA CAG CGA ATT AGG GAT GAA ATT TTG	2132
Arg Gly Gly Glu Gly Asp Val Gly Gln Arg Ile Arg Asp Glu Ile Leu	
665 670 675	
GTC ATC CAG AGG AAC AAT GAC TGC AAG GGT GGT ATG ATG CAA GAA TGG	2180
Val Ile Gln Arg Asn Asn Asp Cys Lys Gly Gly Met Met Gln Glu Trp	
680 685 690	
CAT CAG AAA TTG CAT AAT AAT ACT AGT CCT GAT GAT GTT GTG ATC TGT	2228
His Gln Lys Leu His Asn Asn Thr Ser Pro Asp Asp Val Val Ile Cys	

CAG GCA TTA ATT GAC TAC ATC AAG AGT GAT TTT GAT CTT GGT GTT TAT Gln Ala Leu Ile Asp Tyr Ile Lys Ser Asp Phe Asp Leu Gly Val Tyr 710 715 720	2276
TGG AAA ACC CTG AAT GAG AAC GGA ATA ACA AAA GAG CGT CTT TTG AGT Trp Lys Thr Leu Asn Glu Asn Gly Ile Thr Lys Glu Arg Leu Leu Ser 725 730 735 740	2324
TAT GAC CGT GCT ATC CAT TCT GAA CCA AAT TTT AGA GGA GAT CAA AAG Tyr Asp Arg Ala Ile His Ser Glu Pro Asn Phe Arg Gly Asp Gln Lys 745 750 755	2372
GGT GGT CTT TTG CGT GAT TTA GGT CAC TAT ATG AGA ACA TTG AAG GCA Gly Gly Leu Leu Arg Asp Leu Gly His Tyr Met Arg Thr Leu Lys Ala 760 765 770	2420
GTT CAT TCA GGT GCA GAT CTT GAG TCT GCT ATT GCA AAC TGC ATG GGC Val His Ser Gly Ala Asp Leu Glu Ser Ala Ile Ala Asn Cys Met Gly 775 780 785	2468
TAC AAA ACT GAG GGA GAA GGC TTT ATG GTT GGA GTC CAG ATA AAT CCT Tyr Lys Thr Glu Gly Glu Gly Phe Met Val Gly Val Gln Ile Asn Pro 790 795 800	2516
GTA TCA GGC TTG CCA TCT GGC TTT CAG GAC CTC CTC CAT TTT GTC TTA Val Ser Gly Leu Pro Ser Gly Phe Gln Asp Leu Leu His Phe Val Leu 805 810 815 820	2564
GAC CAT GTG GAA GAT AAA AAT GTG GAA ACT CTT CTT GAG AGA TTG CTA Asp His Val Glu Asp Lys Asn Val Glu Thr Leu Leu Glu Arg Leu Leu 825 830 835	2612
GAG GCT CGT GAG GAG CTT AGG CCC TTG CTT CTC AAA CCA AAC AAC CGT Glu Ala Arg Glu Glu Leu Arg Pro Leu Leu Leu Lys Pro Asn Asn Arg 840 845 850	2660
CTA AAG GAT CTG CTG TTT TTG GAC ATA GCA CTT GAT TCT ACA GTT AGA Leu Lys Asp Leu Leu Phe Leu Asp Ile Ala Leu Asp Ser Thr Val Arg 855 860 865	2708
ACA GCA GTA GAA AGG GGA TAT GAA GAA TTG AAC AAC GCT AAT CCT GAG Thr Ala Val Glu Arg Gly Tyr Glu Glu Leu Asn Asn Ala Asn Pro Glu 870 875 880	2756
AAA ATC ATG TAC TTC ATC TCC CTC GTT CTT GAA AAT CTC GCA CTC TCT Lys Ile Met Tyr Phe Ile Ser Leu Val Leu Glu Asn Leu Ala Leu Ser 885 890 895 900	2804
GTG GAC GAT AAT GAA GAT CTT GTT TAT TGC TTG AAG GGA TGG AAT CAA Val Asp Asp Asn Glu Asp Leu Val Tyr Cys Leu Lys Gly Trp Asn Gln 905 910 915	2852
GCT CTT TCA ATG TCC AAT GGT GGG GAC AAC CAT TGG GCT TTA TTT GCA Ala Leu Ser Met Ser Asn Gly Gly Asp Asn His Trp Ala Leu Phe Ala 920 925 930	2900
AAA GCT GTG CTT GAC AGA ACC CGT CTT GCA CTT GCA AGC AAG GCA GAG Lys Ala Val Leu Asp Arg Thr Arg Leu Ala Leu Ala Ser Lys Ala Glu 935 940 945	2948
TGG TAC CAT CAC TTA TTG CAG CCA TCT GCC GAA TAT CTA GGA TCA ATA Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly Ser Ile	2996

950	955	960	
CTT GGG GTG GAC CAA TGG GCT TTG AAC ATA TTT ACT GAA GAA ATT ATA Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu Ile Ile 965 970 975 980			3044
CGT GCT GGA TCA GCA GCT TCA TTA TCC TCT CTT CTT AAT AGA CTC GAT Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg Leu Asp 985 990 995			3092
CCC GTG CTT CGG AAA ACT GCA AAT CTA GGA AGT TGG CAG ATT ATC AGT Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile Ile Ser 1000 1005 1010			3140
CCA GTT GAA GCC GTT GGA TAT GTT GTC GTT GTG GAT GAG TTG CTT TCA Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp Glu Leu Leu Ser 1015 1020 1025			3188
GTT CAG AAT GAA ATC TAC GAG AAG CCC ACG ATC TTA GTA GCA AAA TCT Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu Val Ala Lys Ser 1030 1035 1040			3236
GTT AAA GGA GAG GAG GAA ATT CCT GAT GGT GCT GTT GCC CTG ATA ACA Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val Ala Leu Ile Thr 1045 1050 1055 1060			3284
CCA GAC ATG CCA GAT GTT CTT TCA CAT GTT TCT GTT CGA GCT AGA AAT Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala Arg Asn 1065 1070 1075			3332
GGG AAG GTT TGC TTT GCT ACA TGC TTT GAT CCC AAT ATA TTG GCT GAC Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn Ile Leu Ala Asp 1080 1085 1090			3380
CTC CAA GCA AAG GAA GGA AGG ATT TTG CTC TTA AAG CCT ACA CCT TCA Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys Pro Thr Pro Ser 1095 1100 1105			3428
GAC ATA ATC TAT AGT GAG GTG AAT GAG ATT GAG CTC CAA AGT TCA AGT Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser Ser Ser 1110 1115 1120			3476
AAC TTG GTA GAA GCT GAA ACT TCA GCA ACA CTT AGA TTG GTG AAA AAG Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val Lys Lys 1125 1130 1135 1140			3524
CAA TTT GGT GGT TGT TAC GCA ATA TCA GCA GAT GAA TTC ACA AGT GAA Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu Phe Thr Ser Glu 1145 1150 1155			3572
ATG GTT GGA GCT AAA TCA CGT AAT ATT GCA TAT CTG AAA GGA AAA GTG Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu Lys Gly Lys Val 1160 1165 1170			3620
CCT TCC TCG GTG GGA ATT CCT ACG TCA GTA GCT CTT CCA TTT GGA GTC Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu Pro Phe Gly Val 1175 1180 1185			3668
TTT GAG AAA GTA CTT TCA GAC GAC ATA AAT CAG GGA GTG GCA AAA GAG Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly Val Ala Lys Glu 1190 1195 1200			3716
TTG CAA ATT CTG ATG AAA AAA CTA TCT GAA GGA GAC TTC AGC GCT CTT			3764

AGA CCA CAG ATG T GATTATATTC TCGTTGTATG TTGTTTCAGAG AAGACCACAG 4537
Arg Pro Gln Met

ATGTGATCAT ATTCTCATTG TATCAGATCT GTGACCACTT ACCTGATACC TCCCATGAAG 4597
TTACCTGTAT GATTATACGT GATCCAAAGC CATCACATCA TGTTCACCTT CAGCTATTGG 4657
AGGAGAAGTG AGAAGTAGGA ATTGCAATAT GAGGAATAAT AAGAAAAACT TTGTAAAAGC 4717
TAAATTAGCT GGGTATGATA TAGGGAGAAA TGTGTAAACA TTGTACTATA TATAGTATAT 4777
ACACACGCAT TATGTATTGC ATTATGCACT GAATAATATC GCAGCATCAA AGAAGAAATC 4837
CTTTGGGTGG TTTCAAAAAA 4856

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1464 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Ser	Asn	Ser	Leu	Gly	Asn	Asn	Leu	Leu	Tyr	Gln	Gly	Phe	Leu	Thr	1	5	10	15
Ser	Thr	Val	Leu	Glu	His	Lys	Ser	Arg	Ile	Ser	Pro	Pro	Cys	Val	Gly	20	25	30	
Gly	Asn	Ser	Leu	Phe	Gln	Gln	Gln	Val	Ile	Ser	Lys	Ser	Pro	Leu	Ser	35	40	45	
Thr	Glu	Phe	Arg	Gly	Asn	Arg	Leu	Lys	Val	Gln	Lys	Lys	Lys	Ile	Pro	50	55	60	
Met	Glu	Lys	Lys	Arg	Ala	Phe	Ser	Ser	Ser	Pro	His	Ala	Val	Leu	Thr	65	70	75	80
Thr	Asp	Thr	Ser	Ser	Glu	Leu	Ala	Glu	Lys	Phe	Ser	Leu	Gly	Gly	Asn	85	90	95	
Ile	Glu	Leu	Gln	Val	Asp	Val	Arg	Pro	Pro	Thr	Ser	Gly	Asp	Val	Ser	100	105	110	
Phe	Val	Asp	Phe	Gln	Val	Thr	Asn	Gly	Ser	Asp	Lys	Leu	Phe	Leu	His	115	120	125	
Trp	Gly	Ala	Val	Lys	Phe	Gly	Lys	Glu	Thr	Trp	Ser	Leu	Pro	Asn	Asp	130	135	140	
Arg	Pro	Asp	Gly	Thr	Lys	Val	Tyr	Lys	Asn	Lys	Ala	Leu	Arg	Thr	Pro	145	150	155	160
Phe	Val	Lys	Ser	Gly	Ser	Asn	Ser	Ile	Leu	Arg	Leu	Glu	Ile	Arg	Asp	165	170	175	
Thr	Ala	Ile	Glu	Ala	Ile	Glu	Phe	Leu	Ile	Tyr	Asp	Glu	Ala	His	Asp	180	185	190	

Lys Trp Ile Lys Asn Asn Gly Gly Asn Phe Arg Val Lys Leu Ser Arg
 195 200 205
 Lys Glu Ile Arg Gly Pro Asp Val Ser Val Pro Glu Glu Leu Val Gln
 210 215 220
 Ile Gln Ser Tyr Leu Arg Trp Glu Arg Lys Gly Lys Gln Asn Tyr Pro
 225 230 235 240
 Pro Glu Lys Glu Lys Glu Glu Tyr Glu Ala Ala Arg Thr Val Leu Gln
 245 250 255
 Glu Glu Ile Ala Arg Gly Ala Ser Ile Gln Asp Ile Arg Ala Arg Leu
 260 265 270
 Thr Lys Thr Asn Asp Lys Ser Gln Ser Lys Glu Glu Pro Leu His Val
 275 280 285
 Thr Lys Ser Asp Ile Pro Asp Asp Leu Ala Gln Ala Gln Ala Tyr Ile
 290 295 300
 Arg Trp Glu Lys Ala Gly Lys Pro Asn Tyr Pro Pro Glu Lys Gln Ile
 305 310 315 320
 Glu Glu Leu Glu Glu Ala Arg Arg Glu Leu Gln Leu Glu Leu Glu Lys
 325 330 335
 Gly Ile Thr Leu Asp Glu Leu Arg Lys Thr Ile Thr Lys Gly Glu Ile
 340 345 350
 Lys Thr Lys Val Glu Lys His Leu Lys Arg Ser Ser Phe Ala Val Glu
 355 360 365
 Arg Ile Gln Arg Lys Lys Arg Asp Phe Gly His Leu Ile Asn Lys Tyr
 370 375 380
 Thr Ser Ser Pro Ala Val Gln Val Gln Lys Val Leu Glu Glu Pro Pro
 385 390 395 400
 Ala Leu Ser Lys Ile Lys Leu Tyr Ala Lys Glu Lys Glu Glu Gln Ile
 405 410 415
 Asp Asp Pro Ile Leu Asn Lys Lys Ile Phe Lys Val Asp Asp Gly Glu
 420 425 430
 Leu Leu Val Leu Val Ala Lys Ser Ser Gly Lys Thr Lys Val His Leu
 435 440 445
 Ala Thr Asp Leu Asn Gln Pro Ile Thr Leu His Trp Ala Leu Ser Lys
 450 455 460
 Ser Pro Gly Glu Trp Met Val Pro Pro Ser Ser Ile Leu Pro Pro Gly
 465 470 475 480
 Ser Ile Ile Leu Asp Lys Ala Ala Glu Thr Pro Phe Ser Ala Ser Ser
 485 490 495
 Ser Asp Gly Leu Thr Ser Lys Val Gln Ser Leu Asp Ile Val Ile Glu
 500 505 510
 Asp Gly Asn Phe Val Gly Met Pro Phe Val Leu Leu Ser Gly Glu Lys
 515 520 525

Val Ala Lys Glu Leu Gln Ile Leu Met Lys Lys Leu Ser Glu Gly Asp
 1205 1210 1215
 Phe Ser Ala Leu Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Ala
 1220 1225 1230
 Pro Ala Gln Leu Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly
 1235 1240 1245
 Met Pro Trp Pro Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp
 1250 1255 1260
 Met Ala Ile Lys Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr
 1265 1270 1275 1280
 Phe Ser Thr Arg Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala
 1285 1290 1295
 Val Leu Val Gln Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His
 1300 1305 1310
 Thr Thr Asn Pro Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val
 1315 1320 1325
 Val Arg Gly Leu Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala
 1330 1335 1340
 Leu Ser Phe Ile Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu
 1345 1350 1355 1360
 Gly Tyr Pro Ser Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile
 1365 1370 1375
 Phe Arg Ser Asp Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala
 1380 1385 1390
 Gly Leu Tyr Asp Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile
 1395 1400 1405
 Asp Tyr Ser Ser Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr
 1410 1415 1420
 Ile Leu Ser Asn Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr
 1425 1430 1435 1440
 Gly Ser Pro Gln Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr
 1445 1450 1455
 Val Val Gln Thr Arg Pro Gln Met
 1460

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1918 base pairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Solanum tuberosum*

(B) STRAIN: C.V. Desiree

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..1555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCA GAG TGG TAC CAT CAC TTA TTG CAG CCA TCT GCC GAA TAT CTA GGA	48
Ala Glu Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly	
1 5 10 15	
TCA ATA CTT GGG GTG GAC CAA TGG GCT TTG AAC ATA TTT ACT GAA GAA	96
Ser Ile Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu	
20 25 30	
ATT ATA CGT GCT GGA TCA GCA GCT TCA TTA TCC TCT CTT CTT AAT AGA	144
Ile Ile Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg	
35 40 45	
CTC GAT CCC GTG CTT CGG AAA ACT GCA AAT CTA GGA AGT TGG CAG ATT	192
Leu Asp Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile	
50 55 60	
ATC AGT CCA GTT GAA GCC GTT GGA TAT GTT GTC GTT GTG GAT GAG TTG	240
Ile Ser Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp Glu Leu	
65 70 75 80	
CTT TCA GTT CAG AAT GAA ATC TAC GAG AAG CCC ACG ATC TTA GTA GCA	288
Leu Ser Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu Val Ala	
85 90 95	
AAA TCT GTT AAA GGA GAG GAG GAA ATT CCT GAT GGT GCT GTT GCC CTG	336
Lys Ser Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val Ala Leu	
100 105 110	
ATA ACA CCA GAC ATG CCA GAT GTT CTT TCA CAT GTT TCT GTT CGA GCT	384
Ile Thr Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala	
115 120 125	
AGA AAT GGG AAG GTT TGC TTT GCT ACA TGC TTT GAT CCC AAT ATA TTG	432
Arg Asn Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn Ile Leu	
130 135 140	
GCT GAC CTC CAA GCA AAG GAA GGA AGG ATT TTG CTC TTA AAG CCT ACA	480
Ala Asp Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys Pro Thr	
145 150 155 160	
CCT TCA GAC ATA ATC TAT AGT GAG GTG AAT GAG ATT GAG CTC CAA AGT	528
Pro Ser Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser	
165 170 175	
TCA AGT AAC TTG GTA GAA GCT GAA ACT TCA GCA ACA CTT AGA TTG GTG	576
Ser Ser Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val	
180 185 190	
AAA AAG CAA TTT GGT GGT TGT TAC GCA ATA TCA GCA GAT GAA TTC ACA	624
Lys Lys Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu Phe Thr	
195 200 205	
AGT GAA ATG GTT GGA GCT AAA TCA CGT AAT ATT GCA TAT CTG AAA GGA	672
Ser Glu Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu Lys Gly	
210 215 220	

AAA GTG CCT TCC TCG GTG GGA ATT CCT ACG TCA GTA GCT CTT CCA TTT Lys Val Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu Pro Phe 225 230 235 240	720
GGA GTC TTT GAG AAA GTA CTT TCA GAC GAC ATA AAT CAG GGA GTG GCA Gly Val Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly Val Ala 245 250 255	768
AAA GAG TTG CAA ATT CTG ACA AAA AAA CTA TCT GAA GGA GAC TTT AGC Lys Glu Leu Gln Ile Leu Thr Lys Lys Leu Ser Glu Gly Asp Phe Ser 260 265 270	816
GCT CTT GGT GAA ATT CGC ACA ACG GTT TTA GAT CTT TCG ACA CCA GCT Ala Leu Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Thr Pro Ala 275 280 285	864
CAA TTG GTC AAA GAG CTG AAG GAG AAG ATG CAG GGT TCT GGC ATG CCT Gln Leu Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly Met Pro 290 295 300	912
TGG CCT GGT GAT GAA GGT CCA AAG CGG TGG GAA CAA GCA TGG ATG GCC Trp Pro Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp Met Ala 305 310 315 320	960
ATA AAA AAG GTG TGG GCT TCA AAA TGG AAT GAG AGA GCA TAC TTC AGC Ile Lys Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr Phe Ser 325 330 335	1008
ACA AGG AAG GTG AAA CTG GAT CAT GAC TAT CTG TGC ATG GCT GTC CTT Thr Arg Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala Val Leu 340 345 350	1056
GTT CAA GAA ATA ATA AAT GCT GAT TAT GCA TTT GTC ATT CAC ACA ACC Val Gln Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His Thr Thr 355 360 365	1104
AAC CCA TCT TCC GGA GAC GAC TCA GAA ATA TAT GCC GAG GTG GTC AGG Asn Pro Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val Val Arg 370 375 380	1152
GGC CTT GGG GAA ACA CTT GTT GGA GCT TAT CCA GGA CGT GCT TTG AGT Gly Leu Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala Leu Ser 385 390 395 400	1200
TTT ATC TGC AAG AAA AAG GAT CTC AAC TCT CCT CAA GTG TTA GGT TAC Phe Ile Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu Gly Tyr 405 410 415	1248
CCA AGC AAA CCG ATC GGC CTT TTC ATA AAA AGA TCT ATC ATC TTC CGA Pro Ser Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile Phe Arg 420 425 430	1296
TCT GAT TCC AAT GGG GAA GAT TTG GAA GGT TAT GCC GGT GCT GGC CTC Ser Asp Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala Gly Leu 435 440 445	1344
TAC GAC AGT GTA CCA ATG GAT GAG GAG GAA AAA GTT GTA ATT GAT TAC Tyr Asp Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile Asp Tyr 450 455 460	1392
TCT TCC GAC CCA TTG ATA ACT GAT GGT AAC TTC CGC CAG ACA ATC CTG Ser Ser Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr Ile Leu 465 470 475 480	1440

TCC AAC ATT GCT CGT GCT GGA CAT GCT ATC GAG GAG CTA TAT GGC TCT	1488
Ser Asn Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr Gly Ser	
485 490 495	
CCT CAA GAC ATT GAG GGT GTA GTG AGG GAT GGA AAG ATT TAT GTC GTT	1536
Pro Gln Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr Val Val	
500 505 510	
CAG ACA AGA CCA CAG ATG T GATTATATTC TCGTTGTATG TTGTTTCAGAG	1585
Gln Thr Arg Pro Gln Met	
515	
AAGACCACAG ATGTGATCAT ATTCTCATTG TATCAGATCT GTGACCACTT ACCTGATACC	1645
TCCCATGAAG TTACCTGTAT GATTATACGT GATCCAAAGC CATCACATCA TGTTACCTT	1705
CAGCTATTGG AGGAGAAAGTG AGAAGTAGGA ATTGCAATAT GAGGAATAAT AAGAAAAACT	1765
TTGTAAAAGC TAAATTAGCT GGGTATGATA TAGGGAGAAA TGTGTAAACA TTGTACTATA	1825
TATAGTATAT ACACACGCAT TATGTATTGC ATTATGCACT GAATAATATC GCAGCATCAA	1885
AGAAGAAATC CTTTGGGTGG TTTCAAAAAA AAA	1918

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 518 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Ala Glu Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly	
1 5 10 15	
Ser Ile Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu	
20 25 30	
Ile Ile Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg	
35 40 45	
Leu Asp Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile	
50 55 60	
Ile Ser Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp Glu Leu	
65 70 75 80	
Leu Ser Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu Val Ala	
85 90 95	
Lys Ser Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val Ala Leu	
100 105 110	
Ile Thr Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala	
115 120 125	
Arg Asn Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn Ile Leu	
130 135 140	
Ala Asp Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys Pro Thr	
145 150 155 160	

Pro Ser Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser
 165 170 175
 Ser Ser Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val
 180 185 190
 Lys Lys Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu Phe Thr
 195 200 205
 Ser Glu Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu Lys Gly
 210 215 220
 Lys Val Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu Pro Phe
 225 230 235 240
 Gly Val Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly Val Ala
 245 250 255
 Lys Glu Leu Gln Ile Leu Thr Lys Lys Leu Ser Glu Gly Asp Phe Ser
 260 265 270
 Ala Leu Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Thr Pro Ala
 275 280 285
 Gln Leu Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly Met Pro
 290 295 300
 Trp Pro Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp Met Ala
 305 310 315 320
 Ile Lys Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr Phe Ser
 325 330 335
 Thr Arg Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala Val Leu
 340 345 350
 Val Gln Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His Thr Thr
 355 360 365
 Asn Pro Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val Val Arg
 370 375 380
 Gly Leu Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala Leu Ser
 385 390 395 400
 Phe Ile Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu Gly Tyr
 405 410 415
 Pro Ser Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile Phe Arg
 420 425 430
 Ser Asp Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala Gly Leu
 435 440 445
 Tyr Asp Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile Asp Tyr
 450 455 460
 Ser Ser Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr Ile Leu
 465 470 475 480
 Ser Asn Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr Gly Ser
 485 490 495

Pro Gln Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr Val Val
500 505 510

Gln Thr Arg Pro Gln Met
515